THE CLAIMS

No claims are amended. However, the presently pending claims are set forth below:

1. (Previously presented) A method of identifying genetically modified mammalian cells expressing a mutated muscle specific tyrosine kinase receptor (mMuSK-R), comprising the steps of:
   a) introducing a nucleic acid sequence encoding a mMuSK-R operatively linked to a promoter into a mammalian cells to form a genetically modified cells;
   b) allowing expression of the mMuSK-R in the genetically modified cells; and
   c) identifying the cells expressing the mMuSK-R.

2. (Previously presented) The method according to claim 1 wherein the mMuSK-R is a mutated form of the amino acid sequence set forth in SEQ ID NO:2.

3. (Original) The method according to claim 1, wherein the mMuSK-R is a sequence having at least 150 amino acids deleted from the intracellular domain of a MuSK-R.

4. (Original) The method according to claim 1, wherein the mMuSK-R is a MuSK-R sequence having the kinase catalytic site deleted.

5. (Previously presented) The method according to claim 3, wherein the mMuSK-R comprises SEQ ID NO:2 wherein amino acids 538-869 or 577-869 are deleted.

6. (Original) The method according to claim 1, wherein the identifying step is accomplished by contacting the genetically modified cells with an antibody.

7. (Previously presented) The method according to claim 1, wherein the nucleic acid sequence encoding the mMuSK-R is introduced into the mammalian cells by a vector.

8. (Original) The method according to claim 6, wherein the vector is a retroviral vector.

9. (Original) The method according to claim 1, wherein the mammalian cells are hematopoietic cells.

10. (Cancelled)

11. (Original) The method according to claim 1, further comprising the step of separating the identified cells expressing the mMuSK-R.

12. (Previously presented) The method according to claim 1, wherein the identifying step comprises separating the genetically modified cells from non-modified cells.

13. (Cancelled)

14. (Previously presented) A method of identifying genetically modified human hematopoietic cells expressing a muscle specific tyrosine kinase receptor (MuSK-R), comprising the steps of:

a) introducing a nucleic acid sequence encoding a MuSK-R into human hematopoietic cells;
b) allowing expression of the MuSK-R in said cells; and
c) identifying the genetically modified hematopoietic cells expressing the MuSK-R.

15-16. (Cancelled)

17. (Previously presented) A method for the immunoselection of transduced mammalian cells expressing a mutated muscle specific tyrosine kinase receptor (mMuSK-R), comprising the steps of:

a) transducing cells with a nucleic acid sequence encoding a mMuSK-R;
b) incubating the cells with an antibody which recognizes and binds to the mMuSK-R; and
c) identifying the bound transduced cells.

18. (Previously presented) The method according to claim 17, wherein the cells are transduced by a retroviral vector derived from moloney murine leukemia virus (MoMLV).

19. (Previously presented) The method according to claim 17, further comprising separating the identified bound transduced cells from non-bound cells.

20. (Previously presented) The method according to claim 17, further comprising expanding the bound transduced cells.

21-24. (Cancelled)

25. (Previously presented) The method according to claim 1, wherein the mMuSK-R is a polypeptide having at least 300 amino acid residues deleted from the cytoplasmic domain of the MuSK-R set forth as SEQ ID NO:2.

26. (Previously presented) The method according to claim 25, wherein the mMuSK-R is a polypeptide having at least amino acid residues 577-869 deleted from the MuSK-R set forth as SEQ ID NO:2.

27. (Previously presented) The method according to claim 17, wherein the mMuSK-R is a polypeptide having at least 300 amino acid residues deleted from the cytoplasmic domain of the MuSK-R set forth as SEQ ID NO:2.

28. (Previously presented) The method according to claim 27, wherein the mMuSK-R is a polypeptide having at least amino acid residues 577-869 deleted from the MuSK-R set forth as SEQ ID NO:2.